

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 17:41:56 ; Search time 1143.19 Seconds
(without alignments)

12714.981 Million cell updates/sec

Title: US-10-623-272-56

Perfect score: 2181

Sequence: 1 CGGCTTACCACACAGCA.....AAGGCTACCATGCAAGGTGA 2181

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: Geneseq2000s.*

4: Geneseq2001as.*

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7: Geneseq2002bs.*

8: Geneseq2003as.*

9: Geneseq2003bs.*

10: Geneseq2003cs.*

11: Geneseq2003ds.*

12: Geneseq2004as.*

13: Geneseq2004bs.*

14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2181	100.0	2181	3	AAD00749 Human Act
2	2169	99.4	4386	4	Aaf54895 Human act
3	2169	99.4	4462	5	ABA83022 Human tra
4	2169	99.4	4663	4	Aa158447 Human pol
5	2169	99.4	4663	5	ADQ98658 DNA encod
6	2169	99.4	4663	9	ADB48418 Novel hum
7	2169	99.4	4713	9	ADA07950 Human act
8	2169	99.4	4713	14	ADX06276 Cyclin-de
9	2165.8	99.3	4193	3	AAD00750 Human Act
10	2140	98.1	4874	2	AAV49807 Human ADN
11	2140	98.1	4874	3	AAV49807 Human act
12	2128.6	97.6	4554	4	AA160233 Human pol
13	1961	89.9	4632	4	Aaf54902 Human act
14	1715.6	78.7	2487	3	AAD00748 Mouse act
15	1697.8	77.8	2421	3	AAV49808 Mouse ADN
16	1697.8	77.8	2421	3	AAD00747 Mouse Act
17	1553	71.2	1766	4	Aa119537 Probe #94
18	1553	71.2	1766	4	ABA64554 Human foe
19	1553	71.2	1766	4	Aa144727 Probe #13

C 20	1553	71.2	1766	4	ABA46681	AbA46681 Human bre
C 21	1553	71.2	1766	4	AAK38731	AAK38731 Human bon
C 22	1553	71.2	1766	4	ABS38306	ABS38306 Human liv
C 23	1553	71.2	1766	5	AA105258	AA105258 Probe #52
C 24	1553	71.2	1766	6	ABS12802	ABS12802 Human gen
25	1103.4	50.6	2420	4	AAK94337	AAK94337 Human ful
26	1103.4	50.6	2420	12	ADL30998	ADL30998 Full leng
27	791.4	36.3	852	4	AAK91980	AAK91980 Human CDN
28	791.4	36.3	852	4	AAK93971	AAK93971 Human CDN
29	791.4	36.3	852	12	ADL30398	ADL30398 5' end of
30	791.4	36.3	852	12	ADL28407	ADL28407 5' end of
31	720.8	33.0	938	2	AAK39926	AAK39926 Gastric c
32	607.4	27.8	772	4	AAK39336	AAK39336 Human CDN
33	607.4	27.8	772	12	ADL29763	ADL29763 5' end of
34	606	27.8	607	4	AAK79209	AAK79209 Human lun
35	606	27.8	607	4	AAK23285	AAK23285 Human lun
36	606	27.8	607	10	ADD66559	ADD66559 Human lun
37	606	27.8	607	10	ADL87813	ADL87813 Human lun
C 38	471	21.6	471	4	AA110258	AA110258 Probe #19
C 39	471	21.6	471	4	ABA51894	ABA51894 Human foe
C 40	471	21.6	471	4	AA131505	AA131505 Probe #19
C 41	471	21.6	471	4	AAK25631	AAK25631 Human bon
C 42	471	21.6	471	4	ABS25208	ABS25208 Human liv
C 43	471	21.6	471	5	AA100195	AA100195 Probe #18
C 44	471	21.6	471	6	ABS00200	ABS00200 Human gen
C 45	395	18.1	396	10	ADD67006	ADD67006 Human lun

ALIGNMENTS

RESULT 1

AAD00749

ID AAD00749 standard; CDNA; 2181 BP.

AC AAD00749;

DT 08-SEP-2000 (first entry)

XX Human Activity Dependent Neurotrophic Factor (ADNF) III H3 CDNA.

DE Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF;

XX Activity Dependent Neuroprotective Protein; chromosome 20q13.2; ADNFLE;

KW Autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;

KW Neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;

KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;

KW epilepsy; AIDS dementia complex; neuropathic pain syndrome; ALS;

KW Amyotrophic lateral sclerosis; Parkinson's disease; Leber's disease;

KW Mitochondrial abnormality; Wernicke's encephalopathy; homocystinuria;

KW Hyperproliferation; sulphite oxide disease; Tourette's syndrome; nontropic;

KW Down's syndrome; drug addiction; developmental retardation; antileptic;

XX learning impairment; anticonvulsant; neuroprotective; anti-HIV; ss.

XX Homo sapiens.

XX Key ... Location/Qualifiers

XX CDS 1..2181

XX FT /*tag= a

XX FT /product= "Human ADNF III H3 protein"

XX FT /transl_except= (pos:997..999, aa:Tyr)

XX FT /note= "Activity Dependent Neurotrophic Factor III"

XX WO200027875-A2.

XX 18-MAY-2000.

XX 04-NOV-1999; 99WO-US026213.

XX 06-NOV-1998; 98US-00187330.

XX (USAS) GOVERNMENT US REPRESENT AS.

XX (UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

Result No.	Query			Length	DB	ID	Description
	Score	Match					
1	42.8	2.0	1452	9	US-10-933-182A-78450	Sequence 78450, A	
2	42.8	2.0	1452	9	US-10-933-182A-78450	Sequence 78450, A	
C 3	41.8	1.9	995	10	US-10-301-480-531242	Sequence 531242, A	
C 4	41.8	1.9	995	10	US-10-301-480-531242	Sequence 531242, A	
5	41.8	1.9	2412	9	US-10-933-182A-6042	Sequence 1144651, A	
6	41.8	1.9	2412	9	US-10-933-182A-6042	Sequence 6042, Ap	
C 7	41	1.9	1020	9	US-10-933-182A-77008	Sequence 6042, Ap	
C 8	41	1.9	1020	9	US-10-933-182A-77008	Sequence 77008, A	
C 9	39.8	1.8	1419	14	US-11-055-822-1095	Sequence 77008, A	
C 10	39.6	1.8	576	6	US-09-925-065A-484403	Sequence 1095, Ap	
C 11	39.4	1.8	609	6	US-09-925-065A-232485	Sequence 484403, A	
12	39.4	1.8	627	10	US-10-301-480-315790	Sequence 232485, A	
13	39.4	1.8	627	10	US-10-301-480-315790	Sequence 315790, A	
14	39.2	1.8	1758	9	US-10-933-182A-76904	Sequence 923199, A	
15	39.2	1.8	1758	9	US-10-933-182A-76904	Sequence 76904, A	
16	39.2	1.8	2787	9	US-10-933-182A-80470	Sequence 80470, A	
17	39.2	1.8	2787	9	US-10-933-182A-80470	Sequence 80470, A	
18	38.8	1.8	564	6	US-09-925-065A-298577	Sequence 298577, A	

DB 877 GC1CCCGAA1ACGAGGAA1G

DB 877 GC1CCCGAA1ACGAGGAA1G

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:11:13 ; Search time 1513.77 Seconds
(without alignments)

11914.334 Million cell updates/sec

Title: US-10-623-272-56

Perfect score: 2181

Sequence: 1 cggctttaccatcacagca.....aaggtaccatgcaaggtga 2181

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2181	100.0	2181	7	US-10-623-272-56
2	2169	99.4	4386	3	US-09-364-609-7
3	2169	99.4	4462	7	US-10-221-625-156
4	2169	99.4	4663	5	US-10-037-270-328
5	2169	99.4	4663	6	US-10-117-722-328
6	2169	99.4	4663	9	US-10-122-851-328
7	2169	99.4	4713	6	US-10-164-432-1
8	2169	99.4	4713	6	US-10-623-272-58
9	2140	98.1	4874	7	US-10-623-272-2
10	1715.6	78.7	2487	7	US-10-623-272-54
11	1697.8	77.8	2421	7	US-10-623-272-4
12	1553	71.2	1766	3	US-09-864-761-30357
13	606	27.8	607	3	US-09-738-973-251
14	606	27.8	607	3	US-09-854-133-251
15	606	27.8	607	5	US-10-144-649A-251
16	471	21.6	471	3	US-09-864-761-13787
17	395	18.1	396	3	US-09-854-133-698
18	395	18.1	396	5	US-10-144-649A-698
19	383.6	17.6	837	7	US-10-623-272-29
20	383.6	17.6	850	7	US-10-623-272-30
21	373.4	17.1	856	5	US-10-060-036-856
22	348.8	16.0	352	3	US-09-777-564-104
23	348.8	16.0	352	5	US-10-015-219-104

Sequence 1874, App
Sequence 7, Appl
Sequence 1152, App
Sequence 9412, App
Sequence 252, App
Sequence 680, App
Sequence 944, App
Sequence 6326, App
Sequence 2312, App
Sequence 4312, App
Sequence 14893, App
Sequence 90597, App
Sequence 2523, App
Sequence 2222, App
Sequence 29690, App
Sequence 600, App
Sequence 346, App
Sequence 1, Appl
Sequence 20772, App

Sequence 1874, App
Sequence 7, Appl
Sequence 1152, App
Sequence 9412, App
Sequence 252, App
Sequence 680, App
Sequence 944, App
Sequence 6326, App
Sequence 2312, App
Sequence 4312, App
Sequence 14893, App
Sequence 90597, App
Sequence 2523, App
Sequence 2222, App
Sequence 29690, App
Sequence 600, App
Sequence 346, App
Sequence 1, Appl
Sequence 20772, App

ALIGNMENTS

RESULT 1
US-10-623-272-56
; Sequence 56, Application US/10623272
; Publication No. US20040053313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Iilana
; APPLICANT: Brennen, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 56
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: ...
; NAME/KEY: ...CDS
; LOCATION: (1)..(2181)
; OTHER INFORMATION: H3 human activity dependent neurotrophic factor
; OTHER INFORMATION: III (ADNF III) clone
US-10-623-272-56

Query Match 100.0%; Score 2181; DB 7; Length 2181;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCTTTTACCATCACAGCAGTGTGATCGACTCTCAATACCAAGCCTAACTTAAT 60
DB 1 CGGCTTTTACCATCACAGCAGTGTGATCGACTCTCAATACCAAGCCTAACTTAAT 60
QY 61 TCTACAGGAGTCAACATGATGTCAGTGTTCATCTGCAGCAGAACCACTATGGAGTCAAA 120
DB 61 TCTACAGGAGTCAACATGATGTCAGTGTTCATCTGCAGCAGAACCACTATGGAGTCAAA 120

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OM nucleic - nucleic search, using sw model
Run on: March 27, 2006, 18:03:33 ; Search time 365.097 Seconds
(without alignments)
10618.724 Million cell updates/sec

Title: US-10-623-272-56
Perfect score: 2181
Sequence: 1 CGGCTTTACCATCACAGCA.....AAGGTACCATGCAAGTGA 2181

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/H COMB.seq.*
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7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2181	100.0	2181	3	US-09-187-330-56
2	2169	99.4	4386	3	US-09-364-609-7
3	2169	99.4	4663	3	US-09-620-312D-328
4	2165.8	99.3	4193	3	US-09-187-330-58
5	2140	98.1	4874	3	US-09-187-330-2
6	1715.6	78.7	2487	3	US-09-187-330-54
7	1697.8	77.8	2421	3	US-09-187-330-4
8	606	27.8	607	3	US-09-370-838-251
9	395	18.1	396	3	US-09-854-133-251
10	383.6	17.6	837	3	US-09-187-330-29
11	383.6	17.6	837	3	US-09-187-330-30
12	215.2	9.9	267	3	US-09-596-569-7
13	215.2	9.9	267	3	US-09-596-569-7
14	55.8	2.6	7218	2	US-08-232-463-14
15	47.2	2.2	3399	3	US-09-614-221A-600
16	44.8	2.1	767677	3	US-09-949-016-12147
17	44.8	2.1	767677	3	US-09-949-016-17361
18	44	2.0	1548	3	US-09-248-796A-6167
19	42	1.9	2277	2	US-08-676-967-2
20	42	1.9	2277	2	US-08-676-974-2
21	42	1.9	2277	2	US-09-098-487-2
22	41.2	1.9	601	3	US-09-949-016-198656
23	40.8	1.9	1664976	3	US-08-916-421B-1
24	40.8	1.9	1664976	3	US-09-692-570-1

c	25	40.6	1.9	505	3	US-09-621-976-15639	Sequence 15639, A
	26	40.2	1.8	4170	3	US-09-976-594-589	Sequence 589, App
	27	40.2	1.8	1664976	3	US-08-916-421B-1	Sequence 1, Appli
	28	40.2	1.8	1664976	3	US-09-692-570-1	Sequence 1, Appli
	29	39.8	1.8	737	4	US-09-605-703B-1245	Sequence 1245, Ap
	30	39.8	1.8	1419	4	US-09-605-703B-1243	Sequence 1243, Ap
	31	39.8	1.8	640681	3	US-09-790-988-1	Sequence 1, Appli
	32	39.6	1.8	1116	3	US-09-248-796A-9660	Sequence 9660, Ap
	33	39.6	1.8	1141	3	US-09-806-708B-22	Sequence 22, Appl
	34	39.6	1.8	7571	3	US-09-949-016-4366	Sequence 4366, Ap
	35	39.6	1.8	8146	3	US-09-976-594-725	Sequence 725, App
	36	39.6	1.8	11917	3	US-09-566-921-32	Sequence 32, Appl
	37	39.6	1.8	101300	3	US-09-949-016-16108	Sequence 16108, A
	38	38.6	1.8	601	3	US-09-949-016-184397	Sequence 184397,
	39	38.6	1.8	580073	3	US-08-545-528D-1	Sequence 1, Appli
	40	38.2	1.8	2672	3	US-09-214-564A-5	Sequence 5, Appli
	41	38.2	1.8	2815	3	US-09-214-564A-1	Sequence 1, Appli
	42	38	1.7	3095	9	5231168-1	Patent No. 5231168
	43	37.8	1.7	2469	3	US-09-328-352-1628	Sequence 1628, Ap
	44	37.8	1.7	31391	3	US-09-949-016-14319	Sequence 14319, A
	45	37.8	1.7	42376	3	US-09-949-016-16276	Sequence 16276, A

ALIGNMENTS

RESULT 1
US-09-187-330-56
; Sequence 56, Application US/09187330
; Patent No. 6613740
; GENERAL INFORMATION:
; APPLICANT: Gozes, Illana
; APPLICANT: Brennenman, Douglas E.
; APPLICANT: Bassean, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/09/187,330
; CURRENT FILING DATE: 1998-11-06
; EARLIER APPLICATION NUMBER: US 60/037,404
; EARLIER FILING DATE: 1997-02-07
; EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 56
; LENGTH: 2181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
; OTHER INFORMATION: H3 human activity dependent neurotrophic factor
; OTHER INFORMATION: III (ADNF III) clone
US-09-187-330-56

QY	1	CGGCTTTTACCATCACAGCAGTGTGATGCCTCTCAATACCAAGCCTTAACCTTAAT	60
DB	1	CGGCTTTTACCATCACAGCAGTGTGATGCCTCTCAATACCAAGCCTTAACCTTAAT	60
QY	61	TTCTACAGAGTCAACATGATGTCAGTGTTCATCTGCAGCAGCAACAACTATGGAGTCAAA	120
DB	61	TTCTACAGAGTCAACATGATGTCAGTGTTCATCTGCAGCAGCAACAACTATGGAGTCAAA	120
QY	121	TTCTGAGGCCAGGGTTACAGTGTTCGTCAGTCAATGAGACTGGTCTAGGTGGCAACGCA	180

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model
Run on: March 27, 2006, 17:54:31 ; Search time 8269.25 Seconds
(without alignments)
12340.003 Million cell updates/sec

Title: US-10-623-272-56
Perfect score: 2181
Sequence: 1 cggcttaccatcacagca.....aaggtaccatgcaaggtga 2181

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_hic:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_est7:*
- 9: gb_ges1:*
- 10: gb_ges2:*
- 11: gb_ges3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2169	99.4	3309	11	DQ049564	DQ049564 Homo sapi
2	2169	99.4	4142	4	HS0800682	AL080163 Homo sapi
3	1762.8	80.8	3309	11	DQ049565	DQ049565 Pan trogl
4	1715.6	78.7	3951	4	BC057666	BC057666 Mus muscu
5	1703.6	78.1	4607	4	BC052455	BC052455 Mus muscu
6	936	42.9	1071	3	BM463769	BM463769 AGENCOURT
7	897.4	41.1	939	7	CR980124	CR980124 CR980124
8	820.8	37.6	1131	3	BM466393	BM466393 AGENCOURT
9	798	36.6	872	6	CD359989	CD359989 AGENCOURT
10	779.2	35.7	784	7	CR388633	CR388633 CR988633
11	772.4	35.4	937	5	BUI58961	BUI58961 AGENCOURT
12	763	35.0	930	8	CV809205	CV809205 AGENCOURT
13	747.2	34.3	2272	4	BC029302	BC029302 Mus muscu
14	738.6	33.9	962	5	BQ963150	BQ963150 AGENCOURT
15	733.2	33.6	794	8	CV756252	CV756252 AGENCOURT
16	714.6	32.8	826	3	DN539719	DN539719 1385527 M
17	703	32.2	915	3	BQ32214	BQ32214 AGENCOURT
18	700.6	32.1	724	1	AW978442	AW978442 EST390551
19	697.6	32.0	875	5	BQ421212	BQ421212 AGENCOURT
20	694	31.8	705	8	CV752173	CV752173 AGENCOURT
21	680	31.2	691	8	CV865793	CV865793 HESCA 6 C
22	678	31.1	817	6	CD657407	CD657407 AGENCOURT

23	677	31.0	864	7	CN646840	CN646840 ILLUMIGEN
24	671	30.8	697	3	BM148883	BM148883 TCAAP2E52
25	670.4	30.7	767	6	CB311734	CB311734 AGENCOURT
26	670.2	30.7	763	5	BW971641	BW971641 BW971641
27	668.4	30.6	681	6	CB155400	CB155400 K-EST0213
28	665.4	30.5	722	2	BE780345	BE780345 601468445
29	665	30.5	900	5	BQ892917	BQ892917 AGENCOURT
30	658	30.2	862	3	BI660703	BI660703 603303525
31	656	30.1	726	7	CN310196	CN310196 170005326
32	654.8	30.0	936	5	BQ887589	BQ887589 AGENCOURT
33	648	29.7	648	6	CB148256	CB148256 K-EST0204
34	645.2	29.6	1140	2	BE886868	BE886868 601513082
35	644.4	29.5	690	2	BE897637	BE897637 601432486
36	642	29.4	744	6	CD110536	CD110536 AGENCOURT
37	640.6	29.4	727	8	DN422175	DN422175 LI84216-0
38	635.2	29.1	753	2	BE872269	BE872269 601446308
39	634.8	29.1	804	8	CK756075	CK756075 AGENCOURT
40	634.2	29.1	691	8	DN378210	DN378210 LI838533
41	630.2	28.9	940	2	EG419378	EG419378 602446062
42	628.8	28.8	797	3	BI684789	BI684789 603307158
43	624.6	28.6	640	7	CR539590	CR539590 DKF2p4591
44	624.2	28.6	726	2	BE257713	BE257713 601114260
45	620.2	28.4	890	2	BG257305	BG257305 602377827

ALIGNMENTS

RESULT 1
DQ049564
LOCUS
DEFINITION Homo sapiens ADNP gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCSSION DQ049564.1 GI:66902763
VERSION DQ049564.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 3309)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 3309)
AUTHORS Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fladel-Alon, A., Tanenbaum, D.M., Civallo, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
FEATURES
source location/Qualifiers
1..3309
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
gene <1..>3309
/gene="ADNP"
ORIGIN
/locus_tag="HC17552"

Query Match 99.4%; Score 2169; DB 11; Length 3309;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2180; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

GenCore version 5.1.7
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Run-on: March 27, 2006, 17:53:30 ; Search time 10581.6 Seconds
(without alignments)
11716.092 Million cell updates/sec

Title: US-10-623-272-56
Perfect score: 2181
Sequence: 1 cggctttaccatcacagca.....aaggctaccatgcaaggtga 2181

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2169	99.4	4386	6 AR430819	Sequence
4	2169	99.4	4386	6 AX081465	Sequence
5	2169	99.4	4462	6 AX274891	Sequence
6	2169	99.4	4663	6 AR338837	Sequence
7	2169	99.4	4682	6 BC090933	Sequence
8	2169	99.4	4713	8 AF250860	Homo sapi
9	2169	99.4	105334	8 HS914P20	Human DNA
10	2165.8	99.3	4193	6 AR392150	Sequence
11	2165.8	99.3	4282	6 AB018327	Homo sapi
12	2165.8	99.3	4942	8 BC075794	Homo sapi
13	2140	98.1	4874	6 BD082199	Activity
14	2140	98.1	4874	6 AR392137	Sequence
15	1961	89.9	4632	6 AX081469	Sequence
16	1895.2	86.9	166118	4 CT009560	Pig DNA s
17	1895.2	86.9	177412	14 CR974565	Sus scrofa
18	1743.2	79.9	172157	14 AC125832	Rattus no

C	19	1743.2	79.9	253693	14	AC093997
	20	1741.6	79.9	2472	9	AF234680
	21	1715.6	78.7	2487	6	AR392148
	22	1715.6	78.7	2487	9	AF068198
	23	1715.6	78.7	4088	9	BC090840
	24	1715.6	78.7	4930	9	AK129214
	25	1715.6	78.7	145263	9	BC005039
	26	1715.6	78.7	186360	14	BC004757
	27	1714	78.6	3846	9	BC050833
	28	1697.8	77.8	2421	6	BD082200
	29	1697.8	77.8	2421	6	AR392138
	30	1553	71.2	1766	6	CQ054429
	31	1553	71.2	1766	6	CQ073670
	32	1553	71.2	1766	6	CQ104554
	33	1553	71.2	1766	6	CQ143266
	34	1553	71.2	1766	6	CQ203099
	35	1553	71.2	1766	6	CQ226457
	36	1553	71.2	1766	6	CQ264598
	37	1553	71.2	1766	6	CQ301688
	38	1103.4	50.6	2420	6	BD127366
	39	1103.4	50.6	2420	6	CQ782891
	40	926.6	42.5	233789	14	AC162696
	41	926.6	42.5	244676	14	AC160170
	42	926.6	37.1	2741	5	CR926295
	43	808.4	36.3	852	6	BD125009
	44	791.4	36.3	852	6	BD127000
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ALIGNMENTS

RESULT 1
LOCUS AR392149 2181 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 56 from patent US 6613740.
ACCESSION AR392149
VERSION AR392149.1 GI:40116053
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2181)
AUTHORS Gozes, I., Breneman, D.B., Bassan, M. and Zamostiano, R.
TITLE Activity dependent neurotrophic factor III (ADNF III)
JOURNAL Patent: US 6613740-A 56 02-SEP-2003;
Ramat University Authority for Applied Research and Industrial
Development Ltd. and The United States of America as represented by
the Secretary of the Department of Health and Human Services; Tel
Aviv;
ILX;

FEATURES
source Location/Qualifiers
1..2181
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN	1	CGGCTTTTACCATCACAGAGATGGTGAATCGACTCTCAATCAACAAAGCCTTAATTAAT	60
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Best Local Similarity	100.0%;	Pred. No. 0;	
Matches 2181;	Conservative	0; Mismatches	0; Indels
			Gaps 0;
Qy	1	CGGCTTTTACCATCACAGAGATGGTGAATCGACTCTCAATCAACAAAGCCTTAATTAAT	60
Db	1	CGGCTTTTACCATCACAGAGATGGTGAATCGACTCTCAATCAACAAAGCCTTAATTAAT	60
Qy	61	TTCTACAGGAGTCAACATGATGTCAGTGTTCATCTCAGCAGAACCACTATGAGTCAAA	120
Db	61	TTCTACAGGAGTCAACATGATGTCAGTGTTCATCTCAGCAGAACCACTATGAGTCAAA	120
Qy	121	TTCTAGGAGGAGGTTTACAGTGTTCAGTCAATGAGACTGGGTCTAGGTGCAACGCA	180
Db	121	TTCTAGGAGGAGGTTTACAGTGTTCAGTCAATGAGACTGGGTCTAGGTGCAACGCA	180

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:29:37 ; Search time 1772.85 Seconds
(without alignments)
.9427.972 Million cell updates/sec

Title: US-10-623-272-58

Perfect score: 4193

Sequence: 1 aaacaggactatcgagca.....gtaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9258654 seqs, 1993127192 residues

Total number of hits satisfying chosen parameters: 18517308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*

- 1: /SIDSS/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SIDSS/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SIDSS/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SIDSS/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 6: /SIDSS/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 10: /SIDSS/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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- 15: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	316.4	7.5	977	10	US-10-301-480-612639
C 2	316.4	7.5	977	10	US-10-301-480-1226048
C 3	48.6	1.2	990	10	US-10-301-480-568793
C 4	48.6	1.2	990	10	US-10-301-480-1182202
C 5	48.6	1.2	11049	8	US-10-240-708-24
C 6	45	1.1	627	6	US-09-925-065A-758867
C 7	44.8	1.1	119036	8	US-10-995-561-13314
C 8	44.6	1.1	2249	11	US-11-068-859-10
C 9	44.6	1.1	2249	11	US-11-068-859-169
C 10	44.6	1.1	2249	11	US-11-068-859-171
C 11	44.4	1.1	942	9	US-10-301-480-85636
C 12	44.4	1.1	942	10	US-10-301-480-699045
C 13	44.4	1.1	992	10	US-10-301-480-551759
C 14	44.4	1.1	992	10	US-10-301-480-1165168
C 15	44.4	1.1	1452	9	US-10-932-182A-78450
C 16	44.4	1.1	1452	9	US-10-932-182A-78450
C 17	44	1.0	667	6	US-09-925-065A-626778
C 18	43.8	1.0	865	11	US-11-246-980-1

C 19	43.8	1.0	865	11	US-11-246-980-12	Sequence 12, Appl
C 20	43.8	1.0	1330	11	US-11-246-980-26	Sequence 26, Appl
C 21	43.8	1.0	1337	11	US-11-246-980-24	Sequence 24, Appl
C 22	43.6	1.0	6801	8	US-10-240-708-61	Sequence 61, Appl
C 23	43.4	1.0	2412	9	US-10-932-182A-6042	Sequence 6042, Ap
C 24	43.4	1.0	2412	9	US-10-932-182A-6042	Sequence 6042, Ap
C 25	43	1.0	2518	8	US-10-947-249-55	Sequence 55, Appl
C 26	42.8	1.0	560	6	US-09-925-065A-12869	Sequence 12869, A
C 27	42.8	1.0	560	9	US-10-301-480-114106	Sequence 114106
C 28	42.8	1.0	560	10	US-10-301-480-727515	Sequence 727515,
C 29	42.8	1.0	985	10	US-10-301-480-575940	Sequence 575940,
C 30	42.8	1.0	985	10	US-10-301-480-1189349	Sequence 1189349,
C 31	42.6	1.0	1366	11	US-11-146-428-7	Sequence 7, Appl1
C 32	42.4	1.0	602	6	US-09-925-065A-894255	Sequence 894255,
C 33	42.2	1.0	990	10	US-10-301-480-568794	Sequence 568794,
C 34	42.2	1.0	990	10	US-10-301-480-1182203	Sequence 1182203,
C 35	42.2	1.0	1766	6	US-09-925-065A-38310	Sequence 38310, A
C 36	42.2	1.0	1766	6	US-09-925-065A-38311	Sequence 38311, A
C 37	42.2	1.0	1766	6	US-09-925-065A-38312	Sequence 38312, A
C 38	42.2	1.0	1766	6	US-09-925-065A-38313	Sequence 38313, A
C 39	42.2	1.0	1766	9	US-10-301-480-139548	Sequence 139548,
C 40	42.2	1.0	1766	9	US-10-301-480-139549	Sequence 139549,
C 41	42.2	1.0	1766	9	US-10-301-480-139550	Sequence 139550,
C 42	42.2	1.0	1766	9	US-10-301-480-139551	Sequence 139551,
C 43	42.2	1.0	1766	10	US-10-301-480-752957	Sequence 752957,
C 44	42.2	1.0	1766	10	US-10-301-480-752958	Sequence 752958,
C 45	42.2	1.0	1766	10	US-10-301-480-752959	Sequence 752959,

ALIGNMENTS

RESULT 1

US-10-301-480-612639/c
; Sequence 612639, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301.480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 612639
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-612639

Query Match: 7.5%; Score 316.4; DB 10; Length 977;

Best Local Similarity 99.7%; Pred. No. 3.7e-68; Indels 0; Gaps 0;
Matches 317; Conservative 0; Mismatches 1;

Qy	3863	AAACAAAACTGGTATTTCAGATCTGTTTCTCAAACTCTTTAAGCTTAAATACATGCA	3922
Db	977	AAACAAAACTGGTATTTCAGATCTGTTTCTCAAACTCTTTAAGCTTAAATACATGCA	918
Qy	3923	AGAATTGACCTTCAGCTACTAAATTTTGACACCTTTTAGATCTGTATAAAGTGTGTGT	3982
Db	917	AGAATTGACCTTCAGCTACTAAATTTTGACACCTTTTAGATCTGTATAAAGTGTGTGT	858
Qy	3983	GTTGAAGCAGCAACCAATGAGTCTGCTGATTTTGGATTTTATCTTTAGTTTCA	4042
Db	857	GTTGAAGCAGCAACCAATGAGTCTGCTGATTTTGGATTTTATCTTTAGTTTCA	798
Qy	4043	CACCATCATGCTGGATTTCATTATACCATCTAATATATATGACACACTTCTTGTATGTAT	4102

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 18:11:13 ; Search time 2910.23 Seconds
(without alignments)
11914.334 Million cell updates/sec

Title: US-10-623-272-58

Perfect score: 4193

Sequence: 1 aaacaggactatcgga.....gtaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
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7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	4177.2	99.6	4462	7	US-10-221-625-156
4	4163.8	99.3	4713	6	US-10-164-432-1
5	4156.6	99.1	4663	5	US-10-037-270-328
6	4156.6	99.1	4663	6	US-10-117-722-328
7	4156.6	99.1	4663	9	US-10-122-851-328
8	3437.2	82.0	4874	7	US-10-623-272-2
9	2165.8	51.7	2181	7	US-10-623-272-56
10	1967.6	46.9	2487	7	US-10-623-272-54
11	1912.8	45.6	2421	7	US-10-623-272-4
12	1762.8	42.0	1766	3	US-09-864-761-30357
13	671	16.0	673	5	US-10-027-632-137463
14	671	16.0	673	6	US-10-027-632-137463
15	642.2	15.3	702	9	US-10-779-543-7881
16	606	14.5	607	3	US-09-738-973-251
17	606	14.5	607	3	US-09-854-133-251
18	606	14.5	607	5	US-10-144-649A-251
19	593	14.1	741	9	US-10-779-543-4311
20	593	14.1	741	9	US-10-779-543-4312
21	547.4	13.1	564	5	US-10-060-036-856
22	544.2	13.0	549	3	US-09-864-761-17004
23	532	12.7	760	9	US-10-779-543-5153

C 24 471 11.2 471 11.2 471 3 US-09-864-761-13787 Sequence 13787, A
C 25 470.2 11.2 475 3 US-09-864-761-179 Sequence 179, App
C 26 450.2 10.7 627 3 US-09-969-034-1152 Sequence 1152, App
27 438.8 10.5 463 7 US-10-242-535A-42054 Sequence 42054, A
28 438.8 10.5 463 7 US-10-085-783A-42054 Sequence 42054, A
29 395.4 9.4 453 3 US-09-918-995-28682 Sequence 28682, A
30 395 9.4 396 3 US-09-854-133-698 Sequence 698, App
31 395 9.4 396 5 US-10-144-649A-698 Sequence 698, App
32 383.6 9.1 837 7 US-10-623-272-29 Sequence 29, Appl
33 383.6 9.1 850 7 US-10-623-272-30 Sequence 30, Appl
34 348.8 8.3 352 3 US-09-777-564-104 Sequence 104, App
35 348.8 8.3 352 5 US-10-015-219-104 Sequence 104, App
36 308.8 7.4 399 3 US-09-960-352-1874 Sequence 1874, App
37 300 7.2 355 7 US-10-242-535A-50957 Sequence 50957, A
38 300 7.2 355 7 US-10-085-783A-50957 Sequence 50957, A
39 286 6.8 300 9 US-10-779-543-944 Sequence 944, App
40 284.2 6.8 300 9 US-10-779-543-942 Sequence 942, App
41 270 6.4 270 3 US-09-796-692-3318 Sequence 3318, App
42 270 6.4 270 3 US-09-796-692-4017 Sequence 4017, App
43 270 6.4 270 5 US-10-040-862-3318 Sequence 3318, App
44 270 6.4 270 5 US-10-040-862-4017 Sequence 4017, App
45 270 6.4 270 6 US-10-057-475B-3318 Sequence 3318, App

ALIGNMENTS

RESULT 1
US-10-623-272-58
; Sequence 58, Application US/10623272
; Publication No. US2004005313A1
; GENERAL INFORMATION:
; APPLICANT: Gozes, Ilana
; APPLICANT: Brennenman, Douglas E.
; APPLICANT: Bassan, Merav
; APPLICANT: Zamostiano, Rachel
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Activity Dependent Neurotrophic Factor III (ADNF III)
; FILE REFERENCE: 015280-291200US
; CURRENT APPLICATION NUMBER: US/10/623,272
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/187,330
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/037,404
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-02-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: WO PCT/US98/02485
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58
; LENGTH: 4193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: ...
; NAME/KEY: CDS
; LOCATION: (492)..(3116)
; OTHER INFORMATION: H7 human activity dependent neurotrophic factor
; OTHER INFORMATION: III (ADNF III) clone
US-10-623-272-58

Query Match 100.0%; Score 4193; DB 7; Length 4193;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAACAGGACTATCGACAAAACCTTCTGTCGAGCGCTTGTCCATTTTCTCAAAAT 60
Db 1 AAACAGGACTATCGACAAAACCTTCTGTCGAGCGCTTGTCCATTTTCTCAAAAT 60
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Db 61 TCTTCTCTGCTACAAAAGTCATTTCGCAATGTCCATAGTGAAGACTTTGAAAATAGGA 120

Result No.	Score	Query Match	Length	DB	ID	Description
1	4193	100.0	4193	3	US-09-187-330-58	Sequence 58, Appl
2	4181.8	99.7	4386	3	US-09-364-608-7	Sequence 7, Appl
3	4156.6	99.1	4663	3	US-09-620-312D-328	Sequence 328, App
4	3437.2	82.0	4874	3	US-09-187-330-2	Sequence 2, Appl
5	2165.8	51.7	2181	3	US-09-187-330-56	Sequence 56, Appl
6	1967.6	46.9	2487	3	US-09-187-330-54	Sequence 54, Appl
7	1912.8	45.6	2421	3	US-09-187-330-4	Sequence 4, Appl
8	606	14.5	607	3	US-09-370-838-251	Sequence 251, App
9	606	14.5	607	3	US-09-854-133-251	Sequence 251, App
10	436.8	10.4	529	3	US-09-306-564-2	Sequence 2, Appl
11	395	9.4	396	3	US-09-854-133-698	Sequence 698, App
12	383.6	9.1	837	3	US-09-187-330-29	Sequence 29, Appl
13	383.6	9.1	850	3	US-09-187-330-30	Sequence 30, Appl
14	215.2	5.1	267	3	US-09-696-569-7	Sequence 7, Appl
15	62.4	1.3	7218	2	US-08-232-463-14	Sequence 14, Appl
16	53.4	1.3	1141	3	US-09-806-708B-22	Sequence 22, Appl
17	50	1.2	50	3	US-09-187-330-61	Sequence 61, Appl
18	49.6	1.2	832	3	US-09-621-976-2813	Sequence 2813, Ap
19	49	1.2	55886	3	US-09-949-016-15129	Sequence 15129, A
20	48.8	1.2	3399	3	US-09-614-221A-600	Sequence 600, App
21	48.4	1.2	50	3	US-09-187-330-63	Sequence 63, Appl
22	48.4	1.2	187169	3	US-09-949-016-12776	Sequence 12776, A
23	48.4	1.2	191569	3	US-09-949-016-15940	Sequence 15940, A
24	47.8	1.1	2238	2	US-08-919-624-2	Sequence 2, Appl

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 17:54:31 ; Search time 15897.7 Seconds
(without alignments)
12340.003 Million cell updates/sec

Title: US-10-623-272-58

Perfect score: 4193

Sequence: 1 aaaccggactatcgagca.....gtaaaaaaaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: EST:

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
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7: gb_est7:*
8: gb_est8:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	3108	74.1	3309	11	DO049564	DO049564 Homo sapi
3	3079.4	73.4	4607	4	BC052455	BC052455 Mus muscu
4	2854.6	68.1	3951	4	BC057666	BC057666 Mus muscu
5	2237.4	53.4	3309	11	DO049565	DO049565 Pan trogl
6	1663	39.7	1671	4	BC015554	BC015554 Homo sapi
7	1346.4	32.1	2272	4	BC029302	BC029302 Mus muscu
8	994.8	23.7	1576	4	AK079160	AK079160 Mus muscu
9	936	22.3	1071	3	BM463769	BM463769 AGENCOURT
10	897.4	21.4	939	7	CR980124	CR980124 CR980124
11	820.8	19.6	1131	3	BM466393	BM466393 AGENCOURT
12	809	19.3	900	5	BQ892917	BQ892917 AGENCOURT
13	798	19.0	872	6	CD359989	CD359989 AGENCOURT
14	793.6	18.9	864	7	CN646840	CN646840 ILLUMINEN
15	782.8	18.7	797	8	CX164702	CX164702 HES2C 19
16	782.2	18.7	949	7	CO647981	CO647981 ILLUMINEN
17	779.2	18.6	784	7	CR988633	CR988633 CR988633
18	769.2	18.3	937	5	BU158961	BU158961 AGENCOURT
19	763	18.2	890	8	CV809205	CV809205 AGENCOURT
20	760	18.1	782	6	CA418550	CA418550 UI-H-E21
21	759.4	18.1	797	3	BM479997	BM479997 AGENCOURT
22	758.2	18.1	1145	2	BG028863	BG028863 602292358

23	751.8	17.9	868	8	DN115885	DN115885.1115411 M
24	751.2	17.9	806	2	BG574926	BG574926.602598012
25	738.6	17.6	962	5	BQ963150	BQ963150. AGENCOURT
26	730.4	17.4	794	8	CK756252	CK756252. AGENCOURT
27	726	17.3	726	7	CN310196	CN310196.170005326
28	718.2	17.1	811	8	DN538297	DN538297.1383991 M
29	714.6	17.0	826	8	DN539719	DN539719.1385527 M
30	713.4	17.0	715	3	BM786807	BM786807. K-EST0065
31	713	17.0	755	6	CA313085	CA313085. UI-CF-FNO
32	711.8	17.0	739	5	BU622230	BU622230. UI-H-FHI-
33	709.8	16.9	774	5	BU732902	BU732902. UI-B-CKI-
34	704.8	16.8	716	6	CB306753	CB306753. UI-CF-FNO
35	703	16.8	915	3	BQ232214	BQ232214. AGENCOURT
36	701.4	16.7	875	5	BQ421212	BQ421212. AGENCOURT
37	701	16.7	722	3	BM678487	BM678487. UI-B-E00-
38	700.6	16.7	724	1	AW978442	AW978442. EST390551
39	700	16.7	820	2	BG615791	BG615791.602643179
40	698.8	16.7	760	8	CK763245	CK763245. AGENCOURT
41	698.2	16.7	801	2	BES35959	BES35959.601062279
42	697.4	16.6	883	8	DN116241	DN116241.1115795 M
43	694	16.6	705	8	CK752173	CK752173. AGENCOURT
44	692.6	16.5	784	7	CO737136	CO737136. SILT02616
45	691.6	16.5	847	7	CV557837	CV557837. UI-N-H20-

ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens mRNA; cDNA DKFZp586K2120 (from clone DKFZp586K2120).
DEFINITION AL080163
ACCESSION AL080163.1 GI:5262626
VERSION HTCC
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4142)
Wambutt, R., Heubner, D., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
The German cDNA Consortium
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764 Neuherberg, GERMANY
COMMENT Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by Agowa (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp586K2120) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp586K2120
Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/
Location/Qualifiers
1. 4142
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/note="activity-dependent neuroprotective protein, N-terminus truncated"
1. 4142
/gene="DKFZp586K2120"
c1. .3018

gene
CDS

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2006, 17:41:56 ; Search time 2197.81 Seconds
(without alignments)
12714.981 Million cell updates/sec

Title: US-10-623-272-58
Perfect score: 4193
Sequence: 1 aaaccaggattatcgga.....gtaaaaaaaaaaaaaa 4193

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4181.8	99.7	4386	4	AAF54895 Human act
3	4177.2	99.6	4462	5	ABA83022 Human tra
4	4163.8	99.3	4713	9	ADA07950 Human act
5	4162.2	99.3	4713	14	ADX06276 Cyclin-de
6	4156.6	99.1	4663	4	AAI58447 Human pol
7	4156.6	99.1	4663	5	ADQ98658 DNA encod
8	4156.6	99.1	4663	9	ADB48418 Novel hum
9	4156.6	99.1	4663	4	AAI60233 Human pol
10	3973.8	94.8	4632	4	AAF54902 Human act
11	3437.2	82.0	4874	2	AAV49807 Human ADN
12	3437.2	82.0	4874	3	AAD00746 Human Act
13	2397.8	57.2	2420	4	AAK94337 Human ful
14	2397.8	57.2	2420	12	ADL30998 Full leng
15	2165.8	51.7	2181	3	AAD00749 Human Act
16	1967.6	46.9	2487	3	AAD00748 Mouse Act
17	1912.8	45.6	2421	2	AAV49808 Mouse ADN
18	1912.8	45.6	2421	3	AAD00747 Mouse Act
19	1762.8	42.0	1766	4	AAI19537 Probe #94

C 20	1762.8	42.0	1766	4	ABA64554	ABA64554 Human foe
C 21	1762.8	42.0	1766	4	AAI44727	AAI44727 Probe #13
C 22	1762.8	42.0	1766	4	ABA46681	ABA46681 Human bre
C 23	1762.8	42.0	1766	4	AAK38731	AAK38731 Human bon
C 24	1762.8	42.0	1766	4	ABS38306	ABS38306 Human liv
C 25	1762.8	42.0	1766	5	AAI05258	AAI05258 Probe #52
C 26	1762.8	42.0	1766	5	ABSI12802	ABSI12802 Human gen
C 27	1762.8	42.0	1766	5	AAK91980	AAK91980 Human CDN
C 28	789.8	18.8	852	4	AAK93971	AAK93971 Human CDN
C 29	789.8	18.8	852	12	ADL30398	ADL30398 5' end of
C 30	789.8	18.8	852	12	ADL28407	ADL28407 5' end of
C 31	721.4	17.2	880	2	AAK39927	AAK39927 Gastric c
C 32	720.8	17.2	838	2	AAK39926	AAK39926 Gastric c
C 33	689.2	16.4	772	4	AAK93336	AAK93336 Human CDN
C 34	689.2	16.4	772	12	ADL29763	ADL29763 5' end of
C 35	642.2	15.3	702	3	AAA01794	AAA01794 Human col
C 36	606	14.5	607	3	AAK79209	AAK79209 Human lun
C 37	606	14.5	607	4	AAK23285	AAK23285 Human lun
C 38	606	14.5	607	10	ADD65559	ADD65559 Human lun
C 39	606	14.5	607	10	ADE87813	ADE87813 Human lun
C 40	605.2	14.4	623	14	ACL55151	ACL55151 Human col
C 41	593	14.1	741	2	AAZ15998	AAZ15998 Human gen
C 42	593	14.1	741	2	AAZ15999	AAZ15999 Human gen
C 43	557.2	13.3	586	4	AAK94032	AAK94032 Human CDN
C 44	557.2	13.3	586	12	ADL30459	ADL30459 3' end of
C 45	547.4	13.1	564	6	ABV95448	ABV95448 Human pan

ALIGNMENTS

RESULT 1
AAD00750
ID AAD00750 standard; cDNA; 4193 BP.
AC AAD00750;
XX
DT 08-SEP-2000 (first entry)
XX Human Activity Dependent Neurotrophic Factor (ADNF) III H7 CDNA.

XX Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF;
KW Activity Dependent Neurotrophic Factor III; ADNF; human; ADNF;
KW autosomal dominant nocturnal frontal-lobe epilepsy; neuronal cell death;
KW neurological deficiency; treatment; HIV; Human Immunodeficiency Virus;
KW Alzheimer's disease; beta-amyloid peptide; Huntington's disease;
KW amyotrophic lateral sclerosis; neuropathic pain syndrome; ALS;
KW mitochondrial abnormality; Wernicke's encephalopathy; homocystinuria;
KW hyperproliferation; sulphite oxide disease; Parkinson's disease; Leber's disease;
KW Down's syndrome; drug addiction; developmental retardation; antileptic;
KW learning impairment; anticonvulsant; neuroprotective; anti-HIV; ss.

OS Homo sapiens.

Key ... Location/Qualifiers
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/*tag= a
/product= "Human ADNF III H7 protein"
/note= "Activity Dependent Neurotrophic Factor III"

WO200027875-A2.

18-MAY-2000.

04-NOV-1999; 99WO-US026213.

06-NOV-1998; 98US-00187330.

(USAS) GOVERNMENT US REPRESENT AS.
(UYRA-) UNIV RAMOT APPLIED RES & IND DEV LTD.

Cozes I, Breneman DE, Bassan M, Zamostiano R;

Result No.	Score	Query Match	Length	DB ID	Description	
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2	4181.8	99.7	4386	6	AX430819	Sequence
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4	4177.2	99.6	4462	6	AX274891	Sequence
5	4174.4	99.6	4682	8	BC090933	Homo sapi
6	4163.8	99.3	4713	8	AF250860	Homo sapi
7	4159	99.2	4282	8	AB018327	Homo sapi
8	4158	99.2	105334	8	HS914P20	Human DNA
9	4156.6	99.1	4663	6	AR338837	Sequence
10	4150.6	99.0	4942	8	BC075794	Homo sapi
11	3973.8	94.8	4632	6	AX081469	Sequence
C 12	3544.2	84.5	166118	4	CT009560	Pig DNA s
C 13	354.2	84.5	177412	14	CR974565	Sus scrofa
14	3437.2	82.0	4874	6	BD082199	activity
15	3437.2	82.0	4874	6	AR392137	Sequence
16	3108	74.1	3314	6	CQ727122	Sequence
17	3092.4	73.8	172157	14	AC125832	Rattus no
C 18	3092.4	73.8	253693	14	AC093997	Rattus no

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33

33